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OIPE

RAW SEQUENCE LISTING
 PATENT APPLICATION: US/10/021,425

DATE: 07/22/2002
 TIME: 09:35:07

Input Set : A:\Pto.amc
 Output Set: N:\CRF3\07222002\J021425.raw

ENTERED

P6

2 <110> APPLICANT: Suzanne L. Bolten
 3 Alan M. Easton
 4 Leslie C. Engel
 5 Dean M. Messing
 6 John S. Ng
 7 Beverly A. Reitz
 8 Scott A. Vaccaro
 9 Mark C. Walker
 10 Ping T. Wang
 11 Robin A. Weinberg
 13 <120> TITLE OF INVENTION: Aspergillus ochraceus 11 alpha
 14 hydroxylase and oxidoreductase
 17 <130> FILE REFERENCE: S03196-00-US
 C--> 19 <140> CURRENT APPLICATION NUMBER: US/10/021,425
 C--> 20 <141> CURRENT FILING DATE: 2001-10-30
 22 <150> PRIOR APPLICATION NUMBER: USSN 60/244,300
 23 <151> PRIOR FILING DATE: 2000-10-30
 25 <160> NUMBER OF SEQ ID NOS: 65
 27 <170> SOFTWARE: FastSEQ for Windows Version 4.0
 29 <210> SEQ ID NO: 1
 30 <211> LENGTH: 1776
 31 <212> TYPE: DNA
 32 <213> ORGANISM: Aspergillus ochraceus
 34 <220> FEATURE:
 35 <221> NAME/KEY: CDS
 36 <222> LOCATION: (146)...(1690)
 37 <223> OTHER INFORMATION: Aspergillus ochraceus 11 alpha hydroxylase
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 40 tggaagtttt tacacttatt atgccggagc cgaaagattc tgagtcgagg ggttggggaa 60
 41 caacactata agacctacaa ccaacttgat ttggtgaatt tacacgggca ttatcaaaac 120
 42 agccacaagc tgacagctca ttatc atg ccc ttc ttc act ggg ctt ctg gcg 172
 43 Met Pro Phe Phe Thr Gly Leu Leu Ala
 44 1 5
 46 att tac cat agt ctc ata ctc gac aac cca gtc caa acc ctg agc acc 220
 47 Ile Tyr His Ser Leu Ile Leu Asp Asn Pro Val Gln Thr Leu Ser Thr
 48 10 15 20 25
 50 att gtc gta ttg gcg gca gcg tac tgg ctc gca acg ctc cag ccg agc 268
 51 Ile Val Val Leu Ala Ala Ala Tyr Trp Leu Ala Thr Leu Gln Pro Ser
 52 30 35 40
 54 gac ctt cct gag ctg aat ccc gcc aaa cca ttc gag ttc acc aat cgt 316
 55 Asp Leu Pro Glu Leu Asn Pro Ala Lys Pro Phe Glu Phe Thr Asn Arg
 56 45 50 55
 58 cgt cgt gtt cat gag ttt gtt gaa aat agt aag agc ttg ctt gct cgg 364

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59	Arg	Arg	Val	His	Glu	Phe	Val	Glu	Asn	Ser	Lys	Ser	Leu	Leu	Ala	Arg	
60			60					65					70				
62	ggg	agg	gaa	ttg	cac	ggg	cac	gag	ccg	tac	aga	ctc	atg	tct	gaa	tgg	412
63	Gly	Arg	Glu	Leu	His	Gly	His	Glu	Pro	Tyr	Arg	Leu	Met	Ser	Glu	Trp	
64		75					80					85					
66	gga	tcc	ttg	att	gtc	ctg	ccc	cca	gag	tgc	gcc	gac	gag	ctg	cgc	aac	460
67	Gly	Ser	Leu	Ile	Val	Leu	Pro	Pro	Glu	Cys	Ala	Asp	Glu	Leu	Arg	Asn	
68	90					95				100						105	
70	gac	cca	aga	atg	gac	ttt	gag	acg	ccc	acc	acc	gac	gac	tcc	cac	gga	508
71	Asp	Pro	Arg	Met	Asp	Phe	Glu	Thr	Pro	Thr	Thr	Asp	Asp	Ser	His	Gly	
72					110					115					120		
74	tat	atc	cct	ggc	ttc	gac	gct	ctc	aac	gca	gac	ccg	aac	ctg	act	aaa	556
75	Tyr	Ile	Pro	Gly	Phe	Asp	Ala	Leu	Asn	Ala	Asp	Pro	Asn	Leu	Thr	Lys	
76				125				130						135			
78	gtg	gtc	acc	aag	tac	ctc	aca	aaa	gca	ttg	aac	aag	ctt	act	gct	ccg	604
79	Val	Val	Thr	Lys	Tyr	Leu	Thr	Lys	Ala	Leu	Asn	Lys	Leu	Thr	Ala	Pro	
80		140						145					150				
82	atc	tcg	cat	gaa	gcg	tcc	atc	gcc	atg	aaa	gcg	gtg	ctg	ggt	gac	gat	652
83	Ile	Ser	His	Glu	Ala	Ser	Ile	Ala	Met	Lys	Ala	Val	Leu	Gly	Asp	Asp	
84		155				160						165					
86	cca	gat	tgg	cgt	gag	atc	tac	cca	gcc	aga	gac	ttg	ctc	cag	ctc	gtc	700
87	Pro	Asp	Trp	Arg	Glu	Ile	Tyr	Pro	Ala	Arg	Asp	Leu	Leu	Gln	Leu	Val	
88	170				175					180					185		
90	gcc	cgg	atg	tcg	aca	aga	gtg	ttc	ctt	ggc	gag	gaa	atg	tgc	aat	aac	748
91	Ala	Arg	Met	Ser	Thr	Arg	Val	Phe	Leu	Gly	Glu	Glu	Met	Cys	Asn	Asn	
92				190						195					200		
94	cag	gat	tgg	atc	caa	acc	tca	tca	caa	tac	gcg	gcc	ctt	gcc	ttc	ggt	796
95	Gln	Asp	Trp	Ile	Gln	Thr	Ser	Ser	Gln	Tyr	Ala	Ala	Leu	Ala	Phe	Gly	
96			205						210					215			
98	gtc	ggt	gac	aag	ctt	aga	ata	tac	ccg	aga	atg	atc	aga	ccg	ata	gta	844
99	Val	Gly	Asp	Lys	Leu	Arg	Ile	Tyr	Pro	Arg	Met	Ile	Arg	Pro	Ile	Val	
100		220						225					230				
102	cat	tgg	ttc	atg	cca	tcc	tgt	tgg	gag	ctg	cgc	cga	tcg	ctg	cga	cgc	892
103	His	Trp	Phe	Met	Pro	Ser	Cys	Trp	Glu	Leu	Arg	Arg	Ser	Leu	Arg	Arg	
104		235				240						245					
106	tgc	cga	cag	att	ctc	acg	ccg	tac	att	cac	aaa	cgc	aag	tcc	ctg	aag	940
107	Cys	Arg	Gln	Ile	Leu	Thr	Pro	Tyr	Ile	His	Lys	Arg	Lys	Ser	Leu	Lys	
108	250				255					260					265		
110	ggg	acc	acg	gac	gag	cag	ggc	aag	ccc	ctt	atg	ttt	gat	gat	tcc	atc	988
111	Gly	Thr	Thr	Asp	Glu	Gln	Gly	Lys	Pro	Leu	Met	Phe	Asp	Asp	Ser	Ile	
112			270							275				280			
114	gag	tgg	ttc	gag	cga	gag	ctg	ggt	ccc	aac	cac	gac	gcg	gtc	ctg	aag	1036
115	Glu	Trp	Phe	Glu	Arg	Glu	Leu	Gly	Pro	Asn	His	Asp	Ala	Val	Leu	Lys	
116			285					290					295				
118	cag	gtc	acg	ctc	tcc	ata	gtt	gct	atc	cac	acc	acg	agt	gac	cta	ctc	1084
119	Gln	Val	Thr	Leu	Ser	Ile	Val	Ala	Ile	His	Thr	Thr	Ser	Asp	Leu	Leu	
120		300						305					310				
122	ttg	cag	gcc	atg	agc	gat	ctc	gcg	cag	aac	ccg	aaa	gtg	cta	caa	gca	1132
123	Leu	Gln	Ala	Met	Ser	Asp	Leu	Ala	Gln	Asn	Pro	Lys	Val	Leu	Gln	Ala	

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124      315      320      325
126 gtc cgc gag gag gtc gtc cga gtc ctg agc acc gag ggg ctc agc aag      1180
127 Val Arg Glu Glu Val Val Arg Val Leu Ser Thr Glu Gly Leu Ser Lys
128 330      335      340      345
130 gtc tcg ctt cac agt ctc aag ctc atg gac agc gcg ttg aag gaa agc      1228
131 Val Ser Leu His Ser Leu Lys Leu Met Asp Ser Ala Leu Lys Glu Ser
132      350      355      360
134 cag cgt ctc agg cct acg ctt ctc ggc tcc ttt cgt cgg cag gca acg      1276
135 Gln Arg Leu Arg Pro Thr Leu Leu Gly Ser Phe Arg Arg Gln Ala Thr
136      365      370      375
138 aat gac atc aag ctg aag agc ggg ttt gtc ata aag aaa ggg act aga      1324
139 Asn Asp Ile Lys Leu Lys Ser Gly Phe Val Ile Lys Lys Gly Thr Arg
140      380      385      390
142 gtc gtc atc gac agc acc cat atg tgg aat ccc gag tat tac act gac      1372
143 Val Val Ile Asp Ser Thr His Met Trp Asn Pro Glu Tyr Tyr Thr Asp
144      395      400      405
146 cct ctc cag tac gac ggg tac cgc tac ttc aac aag cgg cag aca ccc      1420
147 Pro Leu Gln Tyr Asp Gly Tyr Arg Tyr Phe Asn Lys Arg Gln Thr Pro
148 410      415      420      425
150 ggc gag gac aag aac gcg ttg ctc gtc agc aca agc gcc aac cac atg      1468
151 Gly Glu Asp Lys Asn Ala Leu Leu Val Ser Thr Ser Ala Asn His Met
152      430      435      440
154 gga ttc ggt cac ggc gtt cac gcc tgt cct ggc aga ttc ttc gcc tcc      1516
155 Gly Phe Gly His Gly Val His Ala Cys Pro Gly Arg Phe Phe Ala Ser
156      445      450      455
158 aac gag atc aag att gcc ttg tgt cat atc atc tta aat tat gag tgg      1564
159 Asn Glu Ile Lys Ile Ala Leu Cys His Ile Ile Leu Asn Tyr Glu Trp
160      460      465      470
162 cgt ctt cca gac ggc ttc aag ccc cag cct ctc aac atc ggg atg act      1612
163 Arg Leu Pro Asp Gly Phe Lys Pro Gln Pro Leu Asn Ile Gly Met Thr
164      475      480      485
166 tat ctg gcg gat ccc aat acc agg atg ctg atc agg cca cgc aag gcg      1660
167 Tyr Leu Ala Asp Pro Asn Thr Arg Met Leu Ile Arg Pro Arg Lys Ala
168 490      495      500      505
170 gag atc gat atg gcg agt tta act gtg tag gtcgaacacg aagtcctgat      1710
171 Glu Ile Asp Met Ala Ser Leu Thr Val *
172      510
174 gaagtgttat tggtcagtgg gtgaagcaag tcgcagaaat gtgtaacaat ttataagaat      1770
175 aaaaaa      1776
177 <210> SEQ ID NO: 2
178 <211> LENGTH: 514
179 <212> TYPE: PRT
180 <213> ORGANISM: Aspergillus ochraceus
182 <400> SEQUENCE: 2
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184 1      5      10      15
185 Asp Asn Pro Val Gln Thr Leu Ser Thr Ile Val Val Leu Ala Ala Ala
186      20      25      30
187 Tyr Trp Leu Ala Thr Leu Gln Pro Ser Asp Leu Pro Glu Leu Asn Pro

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188          35          40          45
189 Ala Lys Pro Phe Glu Phe Thr Asn Arg Arg Arg Val His Glu Phe Val
190          50          55          60
191 Glu Asn Ser Lys Ser Leu Leu Ala Arg Gly Arg Glu Leu His Gly His
192 65          70          75          80
193 Glu Pro Tyr Arg Leu Met Ser Glu Trp Gly Ser Leu Ile Val Leu Pro
194          85          90          95
195 Pro Glu Cys Ala Asp Glu Leu Arg Asn Asp Pro Arg Met Asp Phe Glu
196          100          105          110
197 Thr Pro Thr Thr Asp Asp Ser His Gly Tyr Ile Pro Gly Phe Asp Ala
198          115          120          125
199 Leu Asn Ala Asp Pro Asn Leu Thr Lys Val Val Thr Lys Tyr Leu Thr
200          130          135          140
201 Lys Ala Leu Asn Lys Leu Thr Ala Pro Ile Ser His Glu Ala Ser Ile
202 145          150          155          160
203 Ala Met Lys Ala Val Leu Gly Asp Asp Pro Asp Trp Arg Glu Ile Tyr
204          165          170          175
205 Pro Ala Arg Asp Leu Leu Gln Leu Val Ala Arg Met Ser Thr Arg Val
206          180          185          190
207 Phe Leu Gly Glu Glu Met Cys Asn Asn Gln Asp Trp Ile Gln Thr Ser
208          195          200          205
209 Ser Gln Tyr Ala Ala Leu Ala Phe Gly Val Gly Asp Lys Leu Arg Ile
210          210          215          220
211 Tyr Pro Arg Met Ile Arg Pro Ile Val His Trp Phe Met Pro Ser Cys
212 225          230          235          240
213 Trp Glu Leu Arg Arg Ser Leu Arg Arg Cys Arg Gln Ile Leu Thr Pro
214          245          250          255
215 Tyr Ile His Lys Arg Lys Ser Leu Lys Gly Thr Thr Asp Glu Gln Gly
216          260          265          270
217 Lys Pro Leu Met Phe Asp Asp Ser Ile Glu Trp Phe Glu Arg Glu Leu
218          275          280          285
219 Gly Pro Asn His Asp Ala Val Leu Lys Gln Val Thr Leu Ser Ile Val
220          290          295          300
221 Ala Ile His Thr Thr Ser Asp Leu Leu Leu Gln Ala Met Ser Asp Leu
222 305          310          315          320
223 Ala Gln Asn Pro Lys Val Leu Gln Ala Val Arg Glu Glu Val Val Arg
224          325          330          335
225 Val Leu Ser Thr Glu Gly Leu Ser Lys Val Ser Leu His Ser Leu Lys
226          340          345          350
227 Leu Met Asp Ser Ala Leu Lys Glu Ser Gln Arg Leu Arg Pro Thr Leu
228          355          360          365
229 Leu Gly Ser Phe Arg Arg Gln Ala Thr Asn Asp Ile Lys Leu Lys Ser
230          370          375          380
231 Gly Phe Val Ile Lys Lys Gly Thr Arg Val Val Ile Asp Ser Thr His
232 385          390          395          400
233 Met Trp Asn Pro Glu Tyr Tyr Thr Asp Pro Leu Gln Tyr Asp Gly Tyr
234          405          410          415
235 Arg Tyr Phe Asn Lys Arg Gln Thr Pro Gly Glu Asp Lys Asn Ala Leu
236          420          425          430

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237 Leu Val Ser Thr Ser Ala Asn His Met Gly Phe Gly His Gly Val His
238           435           440           445
239 Ala Cys Pro Gly Arg Phe Phe Ala Ser Asn Glu Ile Lys Ile Ala Leu
240       450           455           460
241 Cys His Ile Ile Leu Asn Tyr Glu Trp Arg Leu Pro Asp Gly Phe Lys
242 465           470           475           480
243 Pro Gln Pro Leu Asn Ile Gly Met Thr Tyr Leu Ala Asp Pro Asn Thr
244           485           490           495
245 Arg Met Leu Ile Arg Pro Arg Lys Ala Glu Ile Asp Met Ala Ser Leu
246           500           505           510
247 Thr Val
250 <210> SEQ ID NO: 3
251 <211> LENGTH: 2031
252 <212> TYPE: DNA
253 <213> ORGANISM: human
255 <220> FEATURE:
256 <221> NAME/KEY: CDS
257 <222> LOCATION: (1)...(2031)
258 <223> OTHER INFORMATION: human oxidoreductase
260 <400> SEQUENCE: 3
261 atg gga gac tcc cac gtg gac acc agc tcc acc gtg tcc gag gcg gtg      48
262 Met Gly Asp Ser His Val Asp Thr Ser Ser Thr Val Ser Glu Ala Val
263 1           5           10           15
265 gcc gaa gaa gta tct ctt ttc agc atg acg gac atg att ctg ttt tcg      96
266 Ala Glu Glu Val Ser Leu Phe Ser Met Thr Asp Met Ile Leu Phe Ser
267           20           25           30
269 ctc atc gtg ggt ctc cta acc tac tgg ttc ctc ttc aga aag aaa aaa    144
270 Leu Ile Val Gly Leu Leu Thr Tyr Trp Phe Leu Phe Arg Lys Lys Lys
271           35           40           45
273 gaa gaa gtc ccc gag ttc acc aaa att cag aca ttg acc tcc tct gtc    192
274 Glu Glu Val Pro Glu Phe Thr Lys Ile Gln Thr Leu Thr Ser Ser Val
275           50           55           60
277 aga gag agc agc ttt gtg gaa aag atg aag aaa acg ggg agg aac atc    240
278 Arg Glu Ser Ser Phe Val Glu Lys Met Lys Lys Thr Gly Arg Asn Ile
279 65           70           75           80
281 atc gtg ttc tac ggc tcc cag acg ggg act gca gag gag ttt gcc aac    288
282 Ile Val Phe Tyr Gly Ser Gln Thr Gly Thr Ala Glu Glu Phe Ala Asn
283           85           90           95
285 cgc ctg tcc aag gac gcc cac cgc tac ggg atg cga ggc atg tca gcg    336
286 Arg Leu Ser Lys Asp Ala His Arg Tyr Gly Met Arg Gly Met Ser Ala
287           100          105          110
289 gac cct gag gag tat gac ctg gcc gac ctg agc agc ctg cca gag atc    384
290 Asp Pro Glu Glu Tyr Asp Leu Ala Asp Leu Ser Ser Leu Pro Glu Ile
291           115          120          125
293 gac aac gcc ctg gtg gtt ttc tgc atg gcc acc tac ggt gag gga gac    432
294 Asp Asn Ala Leu Val Val Phe Cys Met Ala Thr Tyr Gly Glu Gly Asp
295           130          135          140
297 ccc acc gac aat gcc cag gac ttc tac gac tgg ctg cag gag aca gac    480
298 Pro Thr Asp Asn Ala Gln Asp Phe Tyr Asp Trp Leu Gln Glu Thr Asp

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RAW SEQUENCE LISTING ERROR SUMMARY
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DATE: 07/22/2002
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Input Set : A:\Pto.amc
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Please Note:

Use of n and/or Xaa have been detected in the Sequence Listing. Please review the Sequence Listing to ensure that a corresponding explanation is presented in the <220> to <223> fields of each sequence which presents at least one n or Xaa.

Seq#:11; N Pos. 6,9

Seq#:12; N Pos. 4,10,16